

WHAT IS CLAIMED IS:

- 1 1. An isolated nucleic acid molecule that comprises a polynucleotide
2 sequence that encodes an α 2,3-sialyltransferase polypeptide having an amino acid sequence
3 at least about 75% identical to an amino acid sequence as set forth in SEQ. ID. NO: 2 over a
4 region at least about 50 amino acids in length when compared using the BLASTP algorithm
5 with a wordlength (W) of 3, and the BLOSUM62 scoring matrix.
- 1 2. The nucleic acid of claim 1, wherein the polynucleotide sequence
2 encodes an α 2,3-sialyltransferase having an amino acid sequence as shown in SEQ. ID.
3 NO:2.
- 1 3. The nucleic acid of claim 1, wherein the polynucleotide sequence
2 encodes a α 2,3-sialyltransferase polypeptide having at least about 328 amino acids.
- 1 4. The nucleic acid of claim 3, wherein the polynucleotide sequence
2 encodes a α 2,3-sialyltransferase polypeptide having about 430 amino acids.
- 1 5. The nucleic acid of claim 1, wherein the polynucleotide sequence is at
2 least about 75% identical to a nucleic acid sequence as set forth in SEQ. ID. NO:1 over a
3 region at least about 120 nucleotides in length when compared using the BLASTN algorithm
4 with a wordlength (W) of 11, M=5, and N= -4.
- 1 6. The nucleic acid of claim 1, wherein the polynucleotide sequence
2 hybridizes to a nucleic acid having a sequence as shown in SEQ. ID. NO:1 under stringent
3 conditions.
- 1 7. The nucleic acid of claim 1, wherein the polynucleotide sequence is as
2 shown in SEQ. ID. NO:1.
- 1 8. The nucleic acid of claim 1, wherein the polynucleotide sequence is
2 derived from a *Campylobacter* species.

- 1 9. The nucleic acid of claim 8, wherein the *Campylobacter* species is *C.*
2 *jejuni*.
- 1 10. The nucleic acid of claim 9, wherein the *C. jejuni* is strain OH4384.
- 1 11. The nucleic acid of claim 1, wherein the polynucleotide sequence is
2 operably linked to a second polynucleotide sequence that encodes a second polypeptide.
- 1 12. The nucleic acid of claim 11, wherein the second polypeptide comprises
2 a tag suitable for affinity purification of a fusion protein produced by expression of the
3 nucleic acid.
- 1 13. The nucleic acid of claim 1, further comprising a promoter sequence
2 operably linked to the polynucleotide sequence.
- 1 14. The nucleic acid of claim 13, wherein the promoter is active in
2 eukaryotic cells.
- 1 15. The nucleic acid of claim 13, wherein the promoter is active in
2 prokaryotic cells.
- 1 16. The nucleic acid of claim 15, wherein the promoter is active in *E. coli*.
- 1 17. An isolated nucleic acid molecule which encodes an α 2,3-
2 sialyltransferase polypeptide having an amino acid sequence as shown in SEQ. ID. No. 2.
- 1 18. A cell comprising a recombinant expression cassette containing a
2 promoter operably linked to a polynucleotide sequence which encodes an α 2,3-
3 sialyltransferase polypeptide and which is least about 75% identical to a polynucleotide
4 sequence as set forth in SEQ. ID. NO:1 over a region at least about 120 nucleotides in length
5 when compared using the BLASTN algorithm with a wordlength (W) of 11, M=5, and N= -
6 4.

1 19. The cell of claim 18, wherein the polynucleotide hybridizes to a nucleic
2 acid having a sequence as shown in SEQ. ID. No. 1 under stringent conditions.

1 20. The cell of claim 18, wherein the cell is a prokaryotic cell.

1 21. The cell of claim 20, wherein the cell is *E. coli*.

1 22. The cell of claim 18, wherein the cell is a eukaryotic cell.

1 23. The cell of claim 18, wherein the polynucleotide sequence is as shown
2 in SEQ. ID. No. 1.

1 24. An isolated α 2,3-sialyltransferase polypeptide having an amino acid
2 sequence at least about 75% identical to an amino acid sequence as set forth in SEQ. ID.
3 NO: 2 over a region at least about 50 amino acids in length when compared using the
4 BLASTP algorithm with a wordlength (W) of 3, and the BLOSUM62 scoring matrix.

1 25. The α 2,3-sialyltransferase polypeptide of claim 24 which has at least
2 about 328 amino acids.

1 26. The α 2,3-sialyltransferase polypeptide of claim 24 which has about 430
2 amino acids.

1 27. The α 2,3-sialyltransferase polypeptide of claim 24 which has a
2 sequence as shown in SEQ. ID. NO.: 2.

1 28. A method of adding a sialic acid residue to an acceptor molecule
2 comprising a terminal galactose residue, the method comprising contacting the acceptor
3 molecule with an activated sialic acid molecule and an α 2,3-sialyltransferase having an
4 amino acid sequence at least about 75% identical over a region at least about 50 amino acids
5 in length when compared to the amino acid sequence shown in SEQ. ID. No. 2 using the
6 BLASTP algorithm with a wordlength (W) of 3, and the BLOSUM62 scoring matrix.

1 29. The method of claim 28, wherein the terminal galactose residue is
2 linked through a β linkage to a second residue in the acceptor molecule.

1 30. The method of claim 29, wherein the linkage is a β 1,4 linkage.

1 31. The method of claim 30, wherein the second residue is a Glc or a
2 GlcNAc.

1 32. The method of claim 29, wherein the linkage is a β 1,3 linkage.

1 33. The method of claim 32, wherein the second residue is a GlcNAc or a
2 GalNAc.

1 34. The method of claim 28, wherein the activated sialic acid is CMP-
2 Neu5Ac.